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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 06 17:05:12 EDT 2007

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Application No: 10555669 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-27 08:46:16.101  
Finished: 2007-08-27 08:46:20.722  
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 621 ms  
Total Warnings: 18  
Total Errors: 0  
No. of SeqIDs Defined: 20  
Actual SeqID Count: 20

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)



# SEQUENCE LISTING

<110> WU, TZZY-CHOOU  
HUNG, CHIEN, FU

<120> ANTI-CANCER DNA VACCINE EMPLOYING PLASMIDS ENCODING  
SIGNAL SEQUENCE, MUTANT ONCOPROTEIN ANTIGEN, AND HEAT  
SHOCK PROTEIN

<130> JHV-050.01 (19546-5001)

<140> 10555669

<141> 2007-08-27

<150> PCT/US04/013756

<151> 2004-05-05

<150> 60/467,602

<151> 2003-05-05

<160> 20

<170> PatentIn Ver. 3.3

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<211> 297

<212> DNA

<213> Human papillomavirus

<220>

<221> CDS

<222> (1)..(297)

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cca gag aca act gat ctc tac tgt tat gag caa tta aat gac agc tca	96
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser	
20 25 30	

gag gag gag gat gaa ata gat ggt cca gct gga caa gca gaa ccg gac	144
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp	
35 40 45	

aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt gac tct acg	192
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr	
50 55 60	

ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt act ttg gaa	240
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu	
65 70 75 80	

gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc tgt tct cag	288
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln	

85

90

95

gat aag ctt  
Asp Lys Leu

297

&lt;210&gt; 2

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Human papillomavirus

&lt;400&gt; 2

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln  
1 5 10 15

Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
20 25 30

Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
35 40 45

Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
50 55 60

Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
65 70 75 80

Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln  
85 90 95

Asp Lys Leu

&lt;210&gt; 3

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Human papillomavirus

&lt;400&gt; 3

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln  
1 5 10 15

Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
20 25 30

Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
35 40 45

Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
50 55 60

Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
65 70 75 80

Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln

Lys Pro

<210> 4

<211> 158

<212> PRT

<213> Human papillomavirus

<400> 4

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1 5 10 15

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20 25 30

Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu  
35 40 45

Val Tyr Asp Phe Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly  
50 55 60

Asn Pro Tyr Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile  
65 70 75 80

Ser Glu Tyr Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu  
85 90 95

Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn  
100 105 110

Cys Gln Lys Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp Lys  
115 120 125

Lys Gln Arg Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys Met  
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Ser Cys Cys Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Leu  
145 150 155

<210> 5

<211> 151

<212> PRT

<213> Human papillomavirus

<400> 5

Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu Pro Gln Leu Cys  
1 5 10 15

Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val Tyr  
20 25 30

Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe Arg  
35 40 45

Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys Asp  
50 55 60

Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr Cys  
65 70 75 80

Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro Leu  
85 90 95

Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys Pro  
100 105 110

Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn Ile  
115 120 125

Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg  
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Thr Arg Arg Glu Thr Gln Leu  
145 150

<210> 6

<211> 378

<212> DNA

<213> Human papillomavirus

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tatatgttag atttgcaacc agagacaact gatctctact gttatgagca attaaatgac 180  
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cattacaata ttgtaacctt ttgttgcaag tgtgactcta cgcttcgggt gtgcgtacaa 300  
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<210> 7

<211> 127

<212> PRT

<213> Human papillomavirus

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20 25 30

Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln Pro Glu  
35 40 45

Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu  
50 55 60

Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala

65 70 75 80

His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg  
85 90 95

Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu Asp Leu  
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Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Pro  
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<210> 8

<211> 90

<212> DNA

<213> Human papillomavirus

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<210> 9

<211> 1878

<212> DNA

<213> Mycobacterium tuberculosis

<400> 9

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gcgttcgccc gcaacgggtga ggtgctggtc ggccagccc ccaagaacca ggcagtgacc 180  
aacgtcgatc gcaccgtgctg ctccgtcaag cgacacatgg gcagcgactg gtccatagag 240  
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cgcgacgccg aggcctacct cggtgaggac attaccgacg cggttatcac gacgcccgcc 360  
tacttcaatg acgcccagcg tcaggccacc aaggacgccg gccagatcgc cggcctcaac 420  
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<210> 10

<211> 625

<212> PRT

<213> Mycobacterium tuberculosis

<400> 10

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 20 25 30

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 35 40 45

Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg  
 50 55 60

Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu  
 65 70 75 80

Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu  
 85 90 95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr  
 100 105 110

Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln  
 115 120 125

Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile  
 130 135 140

Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly  
 145 150 155 160

Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe  
 165 170 175

Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala  
 180 185 190

Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val  
 195 200 205

Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Ile Asp Leu  
 210 215 220

Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys  
 225 230 235 240

Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro

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260				265				270							
Leu	Thr	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Asp	Arg
275				280				285							
Thr	Arg	Lys	Pro	Phe	Gln	Ser	Val	Ile	Ala	Asp	Thr	Gly	Ile	Ser	Val
290				295				300							
Ser	Glu	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro
305				310				315				320			
Ala	Val	Thr	Asp	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Lys	Glu	Pro	Asn
325				330				335							
Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln
340				345				350							
Ala	Gly	Val	Leu	Lys	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val
355				360				365							
Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Arg
370				375				380							
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385				390				395				400			
Thr	Thr	Ala	Asp	Asp	Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	Val	Tyr	Gln
405				410				415							
Gly	Glu	Arg	Glu	Ile	Ala	Ala	His	Asn	Lys	Leu	Leu	Gly	Ser	Phe	Glu
420				425				430							
Leu	Thr	Gly	Ile	Pro	Pro	Ala	Pro	Arg	Gly	Ile	Pro	Gln	Ile	Glu	Val
435				440				445							
Thr	Phe	Asp	Ile	Asp	Ala	Asn	Gly	Ile	Val	His	Val	Thr	Ala	Lys	Asp
450				455				460							
Lys	Gly	Thr	Gly	Lys	Glu	Asn	Thr	Ile	Arg	Ile	Gln	Glu	Gly	Ser	Gly
465				470				475				480			
Leu	Ser	Lys	Glu	Asp	Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	Glu	Ala	His
485				490				495							
Ala	Glu	Glu	Asp	Arg	Lys	Arg	Arg	Glu	Glu	Ala	Asp	Val	Arg	Asn	Gln
500				505				510							
Ala	Glu	Thr	Leu	Val	Tyr	Gln	Thr	Glu	Lys	Phe	Val	Lys	Glu	Gln	Arg
515				520				525							
Glu	Ala	Glu	Gly	Gly	Ser	Lys	Val	Pro	Glu	Asp	Thr	Leu	Asn	Lys	Val
530				535				540							
Asp	Ala	Ala	Val	Ala	Glu	Ala	Lys	Ala	Ala	Leu	Gly	Gly	Ser	Asp	Ile

545	550	555	560
Ser Ala Ile Lys Ser Ala Met Glu Lys Leu Gly Gln Glu Ser Gln Ala			
565	570	575	
Leu Gly Gln Ala Ile Tyr Glu Ala Ala Gln Ala Ala Ser Gln Ala Thr			
580	585	590	
Gly Ala Ala His Pro Gly Gly Glu Pro Gly Gly Ala His Pro Gly Ser			
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Ala Asp Asp Val Val Asp Ala Glu Val Val Asp Asp Gly Arg Glu Ala			
610	615	620	

Lys  
625

<210> 11  
<211> 2104  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (1)..(2103)

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cca gag aca act gat ctc tac tgt tat gag caa tta aat gac agc tca	96
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser	
20 25 30	
gag gag gag gat gaa ata gat ggt cca gct gga caa gca gaa ccg gac	144
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp	
35 40 45	
aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt gac tct acg	192
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr	
50 55 60	
ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt act ttg gaa	240
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu	
65 70 75 80	
gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc tgt tct caa	288
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln	
85 90 95	

gga